F6_mel

Global Summary

%DE = 0.22

genes with fdr < 0.2 = 2857 (1770 + / 1087 −)

genes with fdr < 0.1 = 2265 (1438 + / 827 −)

genes with fdr < 0.05 = 1952 (1239 + / 713 −)

genes with fdr < 0.01 = 1268 (821 + / 447 −)

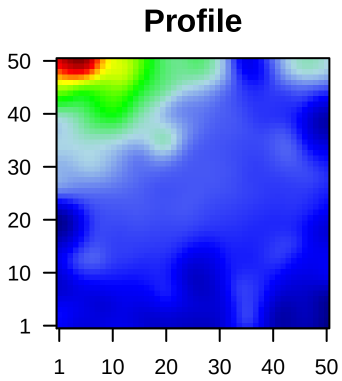
genes in genesets = 14839

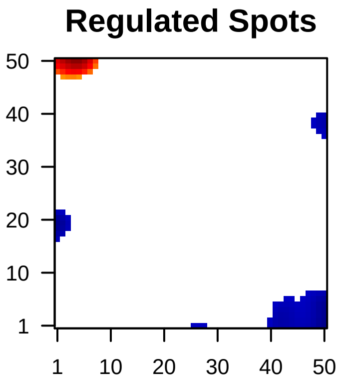
<FC> = 0

<shrinkage−t> = 0.03

<p−value> = 0.07

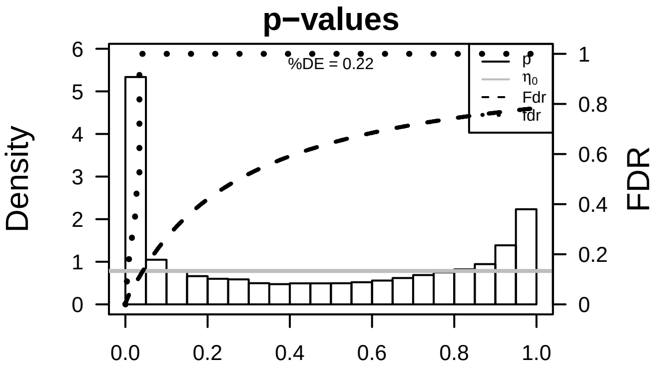
<fdr> = 0.78


Profile


Regulated Spots

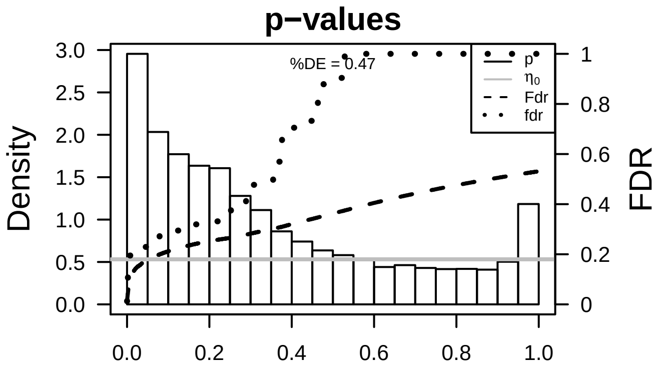
Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	CEP97	2.2	2e−16	1e−13	2 x 47	centrosomal protein 97kDa [Source:HGNC Symbol;Acc:HGN
2	CNOT2	−1.03	2e−16	1e−13	39 x 1	CCR4−NOT transcription complex, subunit 2 [Source:HGNC
3	COL11A1	−1.09	2e−16	1e−13	45 x 1	collagen, type XI, alpha 1 [Source:HGNC Symbol;Acc:HGNC
4	CRYAB	−1.69	2e−16	1e−13	50 x 1	crystallin, alpha B [Source:HGNC Symbol;Acc:HGNC:2389]
5	CRYZL1	−1.55	2e−16	1e−13	44 x 50	crystallin, zeta (quinone reductase)−like 1 [Source:HGNC Sy
6	DCAF13	−1.7	2e−16	1e−13	1 x 1	DDB1 and CUL4 associated factor 13 [Source:HGNC Symbo
7	DFNA5	−1.54	2e−16	1e−13	3 x 18	deafness, autosomal dominant 5 [Source:HGNC Symbol;Acc
8	ELP2	−1.56	2e−16	1e−13	37 x 50	elongator acetyltransferase complex subunit 2 [Source:HGNC
9	HIST1H4C	0.98	2e−16	1e−13	5 x 49	histone cluster 1, H4c [Source:HGNC Symbol;Acc:HGNC:47
10	LAMB2	−1.41	2e−16	1e−13	50 x 6	laminin, beta 2 (laminin S) [Source:HGNC Symbol;Acc:HGNC
11	LGALS1	−1.68	2e−16	1e−13	50 x 1	lectin, galactoside−binding, soluble, 1 [Source:HGNC Symbol
12	MRPS25	−1.4	2e−16	1e−13	2 x 16	mitochondrial ribosomal protein S25 [Source:HGNC Symbol;
13	NCOR1	−1.55	2e−16	1e−13	50 x 18	nuclear receptor corepressor 1 [Source:HGNC Symbol;Acc:H
14	NEMF	−1.73	2e−16	1e−13	47 x 13	nuclear export mediator factor [Source:HGNC Symbol;Acc:H
15	POR	−1.51	2e−16	1e−13	36 x 50	P450 (cytochrome) oxidoreductase [Source:HGNC Symbol;A
16	PSMA5	−1.04	2e−16	1e−13	48 x 50	proteasome (prosome, macropain) subunit, alpha type, 5 [Sou
17	PTK2	−1.66	2e−16	1e−13	32 x 9	protein tyrosine kinase 2 [Source:HGNC Symbol;Acc:HGNC:
18	SF3B1	−1.3	2e−16	1e−13	50 x 36	splicing factor 3b, subunit 1, 155kDa [Source:HGNC Symbol;
19	SNX14	−1.53	2e−16	1e−13	39 x 50	sorting nexin 14 [Source:HGNC Symbol;Acc:HGNC:14977]
20	SOX4	−1.11	2e−16	1e−13	41 x 1	SRY (sex determining region Y)−box 4 [Source:HGNC Symb


p−values

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	20.67	1e−05	242	GSEA C2	KOBAYASHI_EGFR_SIGNALING_24HR_DN
2	20.65	1e−05	305	GSEA C2	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
3	19.51	2e−05	550	GSEA C2	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
4	19.43	2e−05	142	Glio	WILLSCHER_GBM_Verhaak−CL_up (C)
5	18	2e−05	139	GSEA C2	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
6	17.75	2e−05	700	GSEA C2	MARSON_BOUND_BY_E2F4_UNSTIMULATED
7	17.13	3e−05	436	GSEA C2	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
8	17.03	3e−05	155	GSEA C2	HOFFMANN_LARGE_TO_SMALL_PRE_BII_LYMPHOCYTE_UP
9	16.88	3e−05	197	HM	HALLMARK_E2F_TARGETS
10	16.43	4e−05	267	GSEA C2	ZHANG_TLX_TARGETS_60HR_DN
11	16.43	4e−05	145	GSEA C2	CHANG_CYCLING_GENES
12	16.34	4e−05	390	GSEA C2	PUJANA_BRCA2_PCC_NETWORK
13	16.2	4e−05	1192	GSEA C2	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
14	15.86	4e−05	93	GSEA C2	KONG_E2F3_TARGETS
15	15.75	1e−03	16	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
16	15.64	4e−05	96	GSEA C2	CROONQUIST_IL6_DEPRIVATION_DN
17	15.37	5e−05	124	GSEA C2	ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_24HR
18	14.95	5e−05	54	GSEA C2	KANG_DOXORUBICIN_RESISTANCE_UP
19	14.58	6e−05	81	GSEA C2	GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
20	14.57	6e−05	99	GSEA C2	BURTON_ADIPOGENESIS_3
Underexpressed					
1	−6.12	0.002	472	GSEA C2	DUTERTRE_ESTRADIOL_RESPONSE_24HR_DN
2	−5.07	0.003	784	GSEA C2	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_UP
3	−4.98	0.004	3396	Lymphoma	HOPP_Repressed
4	−4.87	0.004	838	Chr	Chr 3
5	−4.69	0.004	548	GSEA C2	NAKAMURA_TUMOR_ZONE_PERIPHERAL_VS_CENTRAL_DN
6	−4.66	0.005	730	GSEA C2	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIA
7	−4.6	0.005	2188	Lymphoma	HOPP_Poised_promoter
8	−4.52	0.005	26	GSEA C2	AKL_HTLV1_INFECTION_UP
9	−4.48	0.005	302	GSEA C2	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_DN
10	−4.45	0.005	749	GSEA C2	CUI_TCF21_TARGETS_2_DN
11	−4.35	0.006	9	GSEA C2	FOURNIER_ACINAR_DEVELOPMENT_LATE_UP
12	−4.35	0.006	137	HM	HALLMARK_UV_RESPONSE_DN
13	−4.29	0.006	1079	Colon Cancer	ZNF_Colon
14	−4.23	0.006	1065	Brain	Overlap_fetal_midbrain_Enh
15	−4.13	0.007	426	GSEA C2	ZWANG_CLASS_1_TRANSIENTLY_INDUCED_BY_EGF
16	−4	0.007	283	GSEA C2	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
17	−3.95	0.008	77	GSEA C2	SWEET_KRAS_TARGETS_UP
18	−3.9	0.008	2563	Lymphoma	HOPP_Heterochrom
19	−3.86	0.008	13	GSEA C2	DAVICIONI_RHABDOMYOSARCOMA_PAX_FOXO1_FUSION_DN
20	−3.83	0.009	129	BP	negative regulation of canonical Wnt signaling pathway


p−values

F6_mel

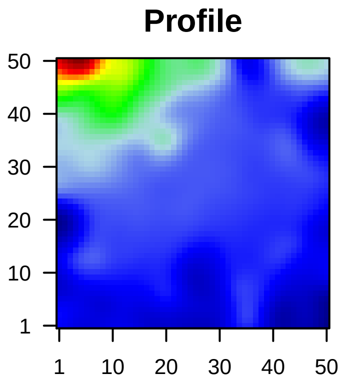
Local Summary

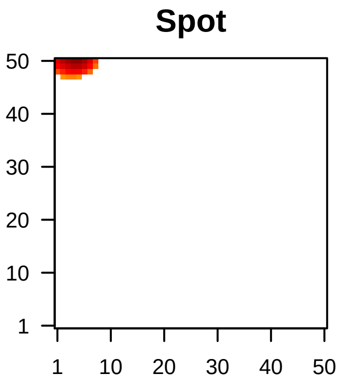
%DE = 0.87
metagenes = 27
genes = 376
genes in genesets = 375

genes with fdr < 0.1 = 292 (270 + / 22 −)
genes with fdr < 0.05 = 269 (253 + / 16 −)
genes with fdr < 0.01 = 228 (218 + / 10 −)

<r> metagenes = 0.92
<r> genes = 0.29

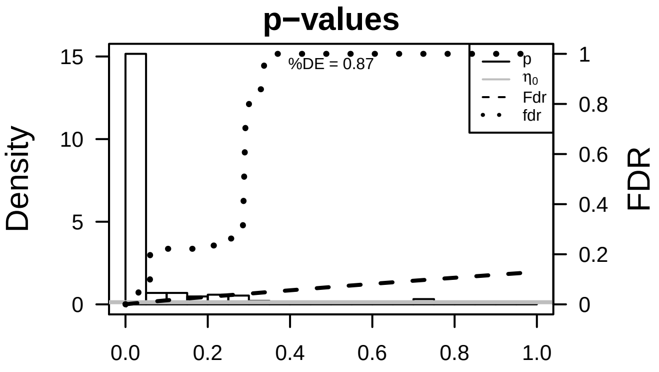
<FC> = 0.63
<shrinkage−t> = 10.14
<p−value> = 0
<fdr> = 0.32





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	CEP97	2.2	2e−16	5e−15	2 x 47	centrosomal protein 97kDa [Source:HGNC Symbol;Acc:HGN
2	HIST1H4C	0.98	2e−16	5e−15	5 x 49	histone cluster 1, H4c [Source:HGNC Symbol;Acc:HGNC:47
3	ARHGEF39	1.79	7e−16	2e−13	6 x 48	Rho guanine nucleotide exchange factor (GEF) 39 [Source:H
4	NUF2	1.79	7e−16	2e−13	6 x 50	NUF2, NDC80 kinetochore complex component [Source:HGN
5	CDK1	1.73	4e−15	1e−12	5 x 50	cyclin−dependent kinase 1 [Source:HGNC Symbol;Acc:HGN
6	HMGB2	1.53	4e−14	1e−12	5 x 50	high mobility group box 2 [Source:HGNC Symbol;Acc:HGNC:
7	RRM2	1.67	5e−14	1e−12	5 x 50	ribonucleotide reductase M2 [Source:HGNC Symbol;Acc:HG
8	NDC80	1.66	7e−14	1e−11	6 x 50	NDC80 kinetochore complex component [Source:HGNC Sym
9	HIST1H1A	1.61	4e−13	1e−11	5 x 49	histone cluster 1, H1a [Source:HGNC Symbol;Acc:HGNC:47
10	TIFA	1.6	5e−13	1e−11	3 x 47	TRAF−interacting protein with forkhead−associated domain [
11	HJURP	1.57	1e−12	1e−11	6 x 50	Holliday junction recognition protein [Source:HGNC Symbol;
12	ANLN	1.57	1e−12	1e−11	5 x 50	anillin, actin binding protein [Source:HGNC Symbol;Acc:HGN
13	FBXO5	1.57	2e−12	1e−11	4 x 50	F−box protein 5 [Source:HGNC Symbol;Acc:HGNC:13584]
14	TOP2A	1.57	2e−12	8e−11	6 x 50	topoisomerase (DNA) II alpha 170kDa [Source:HGNC Symbo
15	MELK	1.54	3e−12	8e−11	5 x 50	maternal embryonic leucine zipper kinase [Source:HGNC Sy
16	UBE2C	1.52	6e−12	8e−11	6 x 50	ubiquitin−conjugating enzyme E2C [Source:HGNC Symbol;
17	ZWINT	1.49	8e−12	8e−11	5 x 50	ZW10 interacting kinetochore protein [Source:HGNC Symbol
18	ZNF143	1.51	9e−12	8e−11	5 x 50	zinc finger protein 143 [Source:HGNC Symbol;Acc:HGNC:12
19	PBK	1.51	1e−11	2e−10	6 x 50	PDZ binding kinase [Source:HGNC Symbol;Acc:HGNC:1828
20	SPC25	1.5	1e−11	2e−10	6 x 50	SPC25, NDC80 kinetochore complex component [Source:HG



F6_mel

Local Summary

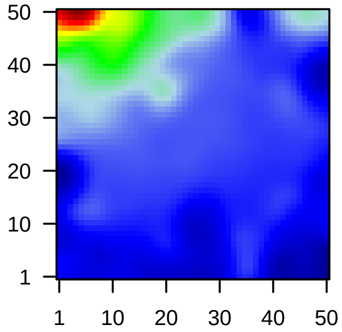
%DE = 0.61
metagenes = 3
genes = 82
genes in genesets = 81

genes with fdr < 0.1 = 15 (5 + / 10 −)
genes with fdr < 0.05 = 7 (3 + / 4 −)
genes with fdr < 0.01 = 2 (1 + / 1 −)

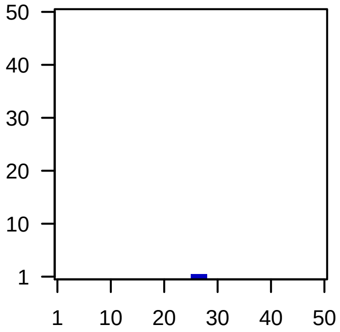
<r> metagenes = 0.99
<r> genes = 0.27

<FC> = −0.17
<shrinkage−t> = −2.63
<p−value> = 0.11
<fdr> = 0.82

Profile



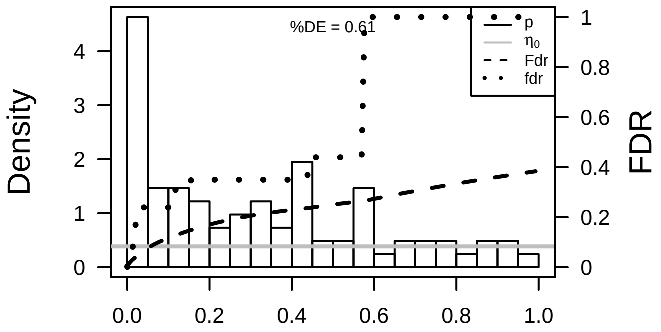
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	MMS19	0.94	2e−05	0.001	28 x 1	MMS19 nucleotide excision repair homolog (S. cerevisiae) [S
2	AKIRIN1	−0.88	8e−05	0.001	28 x 1	akirin 1 [Source:HGNC Symbol;Acc:HGNC:25744]
3	ARIH1	−0.86	1e−04	0.011	26 x 1	ariadne RBR E3 ubiquitin protein ligase 1 [Source:HGNC Sy
4	KLF6	0.69	5e−04	0.011	27 x 1	Kruppel−like factor 6 [Source:HGNC Symbol;Acc:HGNC:223
5	NRAS	0.74	9e−04	0.011	27 x 1	neuroblastoma RAS viral (v−ras) oncogene homolog [Source
6	ANP32A	−0.72	1e−03	0.012	26 x 1	acidic (leucine−rich) nuclear phosphoprotein 32 family, memb
7	ETS1	−0.71	1e−03	0.021	28 x 1	v−ets avian erythroblastosis virus E26 oncogene homolog 1 [
8	NUS1	0.68	2e−03	0.053	28 x 1	nuclear undecaprenyl pyrophosphate synthase 1 homolog (S.
9	BOD1L1	−0.64	4e−03	0.053	28 x 1	biorientation of chromosomes in cell division 1−like 1 [Source
10	UBE2E1	−0.61	6e−03	0.053	27 x 1	ubiquitin−conjugating enzyme E2E 1 [Source:HGNC Symbol;
11	MAF1	−0.6	7e−03	0.073	27 x 1	MAF1 homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:H
12	TLE1	0.56	1e−02	0.073	26 x 1	transducin−like enhancer of split 1 (E(sp1) homolog, Drosoph
13	KRT10	−0.55	1e−02	0.073	26 x 1	keratin 10, type I [Source:HGNC Symbol;Acc:HGNC:6413]
14	BRAF	−0.54	1e−02	0.098	28 x 1	B−Raf proto−oncogene, serine/threonine kinase [Source:HG
15	PACS2	−0.52	2e−02	0.098	28 x 1	phosphofurin acidic cluster sorting protein 2 [Source:HGNC
16	SCAF8	−0.52	2e−02	0.187	26 x 1	SR−related CTD−associated factor 8 [Source:HGNC Symbol;
17	PRKCE	−0.48	3e−02	0.187	27 x 1	protein kinase C, epsilon [Source:HGNC Symbol;Acc:HGNC:
18	ARNT	−0.47	3e−02	0.187	27 x 1	aryl hydrocarbon receptor nuclear translocator [Source:HGN
19	MAML2	−0.46	4e−02	0.239	26 x 1	mastermind−like 2 (Drosophila) [Source:HGNC Symbol;Acc:
20	EP300	−0.42	6e−02	0.239	27 x 1	E1A binding protein p300 [Source:HGNC Symbol;Acc:HGNC

p−values



F6_mel

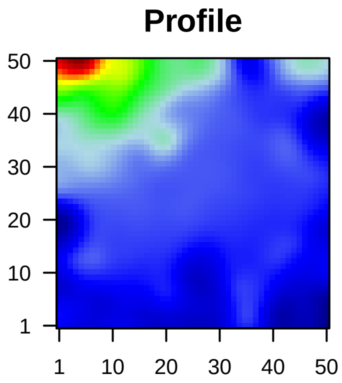
Local Summary

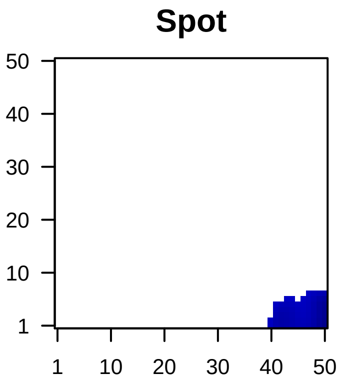
%DE = 0.67
metagenes = 63
genes = 690
genes in genesets = 689

genes with fdr < 0.1 = 263 (76 + / 187 −)
genes with fdr < 0.05 = 192 (55 + / 137 −)
genes with fdr < 0.01 = 123 (36 + / 87 −)

<r> metagenes = 0.86
<r> genes = 0.13

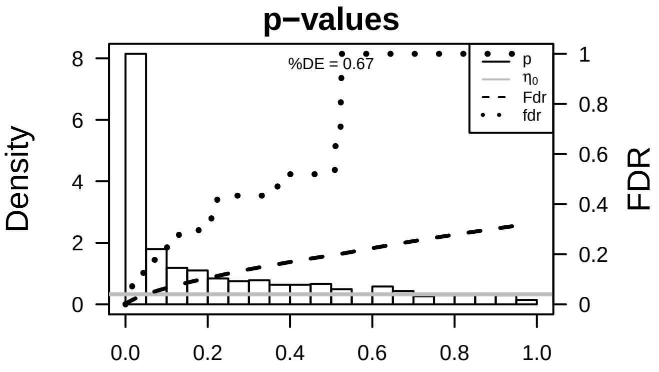
<FC> = −0.18
<shrinkage−t> = −3.01
<p−value> = 0.02
<fdr> = 0.68





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	COL11A1	−1.09	2e−16	1e−14	45 x 1	collagen, type XI, alpha 1 [Source:HGNC Symbol;Acc:HGNC
2	CRYAB	−1.69	2e−16	1e−14	50 x 1	crystallin, alpha B [Source:HGNC Symbol;Acc:HGNC:2389]
3	LAMB2	−1.41	2e−16	1e−14	50 x 6	laminin, beta 2 (laminin S) [Source:HGNC Symbol;Acc:HGNC
4	LGALS1	−1.68	2e−16	1e−14	50 x 1	lectin, galactoside−binding, soluble, 1 [Source:HGNC Symbol
5	SOX4	−1.11	2e−16	1e−14	41 x 1	SRY (sex determining region Y)−box 4 [Source:HGNC Symbo
6	C5orf15	−1.49	4e−16	2e−11	48 x 5	chromosome 5 open reading frame 15 [Source:HGNC Symbo
7	PLK2	−1.23	1e−13	3e−11	50 x 1	polo−like kinase 2 [Source:HGNC Symbol;Acc:HGNC:19699]
8	TM2D1	−1.42	3e−13	4e−11	42 x 1	TM2 domain containing 1 [Source:HGNC Symbol;Acc:HGNC
9	LRRFIP2	−1.4	5e−13	4e−11	50 x 4	leucine rich repeat (in FLII) interacting protein 2 [Source:HGN
10	CDKN1A	1.59	6e−13	5e−09	50 x 1	cyclin−dependent kinase inhibitor 1A (p21, Cip1) [Source:HG
11	CALD1	−0.94	3e−11	5e−09	50 x 1	caldesmon 1 [Source:HGNC Symbol;Acc:HGNC:1441]
12	ANKZF1	1.46	4e−11	1e−08	47 x 1	ankyrin repeat and zinc finger domain containing 1 [Source:H
13	DYNC1LI1	−1.26	2e−10	1e−08	47 x 1	dynein, cytoplasmic 1, light intermediate chain 1 [Source:HGN
14	LAMC1	−1.26	2e−10	1e−08	50 x 3	laminin, gamma 1 (formerly LAMB2) [Source:HGNC Symbol;
15	TBL1XR1	−0.93	2e−10	1e−07	50 x 5	transducin (beta)−like 1 X−linked receptor 1 [Source:HGNC S
16	AKR1A1	−1.25	1e−09	1e−07	50 x 7	aldo−keto reductase family 1, member A1 (aldehyde reductas
17	SULF2	1.33	2e−09	1e−07	50 x 3	sulfatase 2 [Source:HGNC Symbol;Acc:HGNC:20392]
18	ACOT9	−1.23	2e−09	1e−07	47 x 1	acyl−CoA thioesterase 9 [Source:HGNC Symbol;Acc:HGNC:
19	CCNL2	−1.21	3e−09	1e−07	45 x 4	cyclin L2 [Source:HGNC Symbol;Acc:HGNC:20570]
20	STAM	−1.19	3e−09	1e−07	50 x 3	signal transducing adaptor molecule (SH3 domain and ITAM



F6_mel

Local Summary

%DE = 0.69

metagenes = 14

genes = 248

genes in genesets = 247

genes with fdr < 0.1 = 101 (16 + / 85 −)

genes with fdr < 0.05 = 83 (15 + / 68 −)

genes with fdr < 0.01 = 59 (9 + / 50 −)

<r> metagenes = 0.96

<r> genes = 0.15

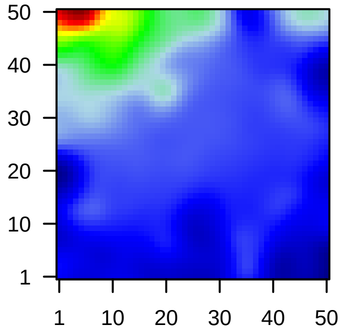
<FC> = −0.25

<shrinkage−t> = −4.16

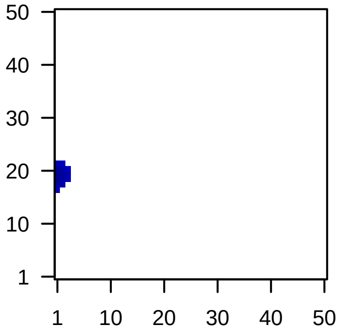
<p−value> = 0.01

<fdr> = 0.61

Profile



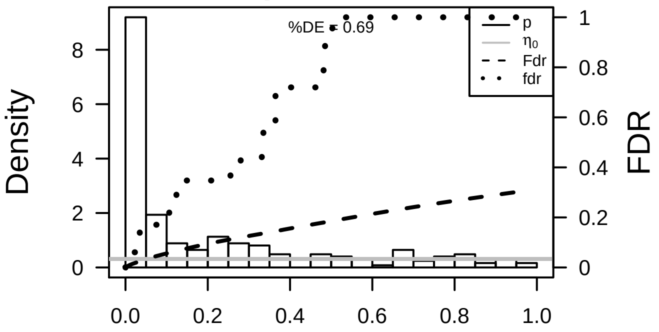
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	PTPN2	−1.33	7e−12	4e−08	1 x 20	protein tyrosine phosphatase, non−receptor type 2 [Source:H
2	LMNA	−0.9	5e−10	5e−07	2 x 19	lamin A/C [Source:HGNC Symbol;Acc:HGNC:6636]
3	HMG20B	−1.02	7e−09	2e−06	1 x 20	high mobility group 20B [Source:HGNC Symbol;Acc:HGNC:5
4	MRPS26	−1.13	3e−08	2e−06	1 x 21	mitochondrial ribosomal protein S26 [Source:HGNC Symbol;
5	FTH1	−0.49	6e−08	3e−06	1 x 21	ferritin, heavy polypeptide 1 [Source:HGNC Symbol;Acc:HGN
6	MOK	−1.07	1e−07	3e−06	1 x 21	MOK protein kinase [Source:HGNC Symbol;Acc:HGNC:9833
7	NT5C3B	−1.15	1e−07	3e−06	1 x 20	5'−nucleotidase, cytosolic IIIB [Source:HGNC Symbol;Acc:H
8	SNF8	−0.86	2e−07	3e−06	1 x 21	SNF8, ESCRT−II complex subunit [Source:HGNC Symbol;Ac
9	IMP3	−1.03	3e−07	3e−06	1 x 22	IMP3, U3 small nucleolar ribonucleoprotein [Source:HGNC S
10	DGUOK	−0.79	3e−07	3e−05	3 x 20	deoxyguanosine kinase [Source:HGNC Symbol;Acc:HGNC:
11	PRCP	−1.07	1e−06	3e−05	1 x 19	prolylcarboxypeptidase (angiotensinase C) [Source:HGNC S
12	SERPINE2	−1.07	1e−06	3e−05	1 x 20	serpin peptidase inhibitor, clade E (nexin, plasminogen activa
13	HEXB	−0.91	1e−06	8e−05	1 x 21	hexosaminidase B (beta polypeptide) [Source:HGNC Symbol
14	SLC11A2	−1.03	4e−06	8e−05	1 x 20	solute carrier family 11 (proton−coupled divalent metal ion tra
15	SETD4	1.02	4e−06	8e−05	1 x 22	SET domain containing 4 [Source:HGNC Symbol;Acc:HGNC
16	APPL1	−0.92	5e−06	8e−05	1 x 21	adaptor protein, phosphotyrosine interaction, PH domain and
17	SURF1	−1.01	6e−06	8e−05	1 x 18	surfeit 1 [Source:HGNC Symbol;Acc:HGNC:11474]
18	PRELID1	−0.93	6e−06	8e−05	1 x 20	PRELI domain containing 1 [Source:HGNC Symbol;Acc:HGN
19	C17orf89	−0.99	8e−06	8e−05	1 x 21	chromosome 17 open reading frame 89 [Source:HGNC Sym
20	SCARB1	−0.81	8e−06	2e−04	2 x 20	scavenger receptor class B, member 1 [Source:HGNC Symb

p−values



F6_mel

Local Summary

%DE = 0.63

metagenes = 11

genes = 144

genes in genesets = 143

genes with fdr < 0.1 = 60 (15 + / 45 −)

genes with fdr < 0.05 = 60 (15 + / 45 −)

genes with fdr < 0.01 = 34 (8 + / 26 −)

<r> metagenes = 0.97

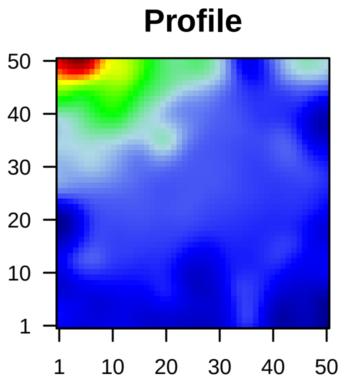
<r> genes = 0.09

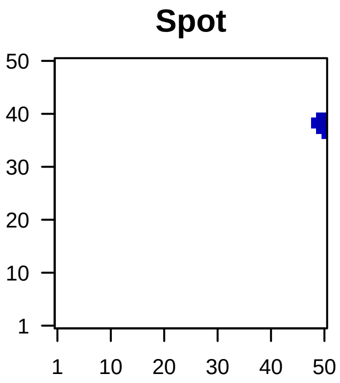
<FC> = −0.22

<shrinkage−t> = −3.86

<p−value> = 0.01

<fdr> = 0.57





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	SF3B1	−1.3	2e−16	1e−14	50 x 36	splicing factor 3b, subunit 1, 155kDa [Source:HGNC Symbol;
2	MRPL3	−1.01	3e−12	1e−10	50 x 37	mitochondrial ribosomal protein L3 [Source:HGNC Symbol;A
3	WDR45	−1.35	5e−12	5e−09	50 x 39	WD repeat domain 45 [Source:HGNC Symbol;Acc:HGNC:28
4	RPUSD3	−1.31	1e−10	5e−09	50 x 39	RNA pseudouridylate synthase domain containing 3 [Source:
5	UBXN1	−0.75	2e−10	2e−08	50 x 39	UBX domain protein 1 [Source:HGNC Symbol;Acc:HGNC:18
6	LTV1	−1.26	6e−10	2e−07	50 x 36	LTV1 ribosome biogenesis factor [Source:HGNC Symbol;Acc
7	SMOX	1.3	4e−09	7e−06	49 x 40	spermine oxidase [Source:HGNC Symbol;Acc:HGNC:15862]
8	RNFT1	−1.15	1e−07	1e−05	50 x 39	ring finger protein, transmembrane 1 [Source:HGNC Symbol;
9	DENND4A	1.13	4e−07	1e−05	50 x 38	DENN/MADD domain containing 4A [Source:HGNC Symbol;
10	FER	−1.09	6e−07	3e−05	50 x 39	fer (fps/fes related) tyrosine kinase [Source:HGNC Symbol;A
11	GOSR1	−0.99	1e−06	3e−05	50 x 39	golgi SNAP receptor complex member 1 [Source:HGNC Sym
12	PLIN3	−1.04	2e−06	3e−05	49 x 40	perilipin 3 [Source:HGNC Symbol;Acc:HGNC:16893]
13	NUDT9	1.05	2e−06	5e−05	50 x 40	nudix (nucleoside diphosphate linked moiety X)−type motif 9
14	FEZ2	1.03	3e−06	5e−05	49 x 40	fasciculation and elongation protein zeta 2 (zygin II) [Source:
15	VPS45	−1.02	4e−06	1e−04	50 x 39	vacuolar protein sorting 45 homolog (S. cerevisiae) [Source:
16	HACL1	−0.99	8e−06	1e−04	50 x 39	2−hydroxyacyl−CoA lyase 1 [Source:HGNC Symbol;Acc:HG
17	RGS3	−0.99	8e−06	1e−04	50 x 40	regulator of G−protein signaling 3 [Source:HGNC Symbol;Ac
18	MTO1	−0.98	1e−05	3e−04	50 x 39	mitochondrial tRNA translation optimization 1 [Source:HGNC
19	TMEM173	0.94	2e−05	3e−04	50 x 38	transmembrane protein 173 [Source:HGNC Symbol;Acc:HG
20	FBXO38	0.93	3e−05	3e−04	50 x 38	F−box protein 38 [Source:HGNC Symbol;Acc:HGNC:28844]